AMENDMENTS TO THE CLAIMS

Claim 1 (Currently amended): A method of determining statistical significance of disease incidence, said method comprising:

~~a.~~a) selecting at least one founder from a computerized genealogical database;

~~b.~~b) identifying a very large family from the founder in said computerized genealogical database;

~~c.~~c) linking the very large family to a disease database;

~~d.~~d) determining an incidence of disease by calculating which and how many individuals within the very large family have the disease;

~~e.~~e) comparing the incidence of disease in the very large family to a general population incidence of disease; and

~~f.~~f) assessing a statistical significance of the disease incidence in the very large family and presenting a measure of said statistical significance on a display or printout.

Claim 2 (Original): A method as in claim 1, comprising:
determining a relative risk of incidence of disease for the very large family.

Claim 3 (Original): A method as in claim 2, comprising:
determining a relative risk of incidence of disease for an individual within the very large family.

Claim 4 (Original): A method as in claim 1, comprising:
obtaining DNA samples from individuals with disease and their family within the very large family.

Claim 5 (Original): A method as in claim 4 comprising:
identifying identity-by-decent regions within the DNA samples.

Claim 6 (Original): A method as in claim 5, comprising:
identifying a susceptibility gene within the identity-by-descent regions.

Claim 7 (Original): A method comprising:

determining relative risk of incidence of disease for a very large family.

Claim 8 (Original): A method as in claim 7, comprising:

determining a relative risk of incidence of disease for an individual withn the very large family.

Claims 9-10 (Canceled).